MAR 130 69 1995 6

SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: Lobb, Roy R.
- (ii) TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 60 State Street, Suite 510
 - (C) CITY Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: \ IBM PC compatible
 - (C) OPERATING \SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/373,857
 - (B) FILING DATE: \18 JAN 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/284,603
 - (B) FILING DATE: 11-AUG-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: US 07/835,139
 - (B) FILING DATE: 12 FEB 1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: ACT/US93/00924
 - (B) FILING DATE: 2-FEB-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Louis Myers (PLM)
 - (B) REGISTRATION NUMBER: 35\965
 (C) REFERENCE/DOCKET NUMBER:\BGP-031USCP
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid

STRANDEDNESS: single TOPOLOGY: linear (ii) MOLEQULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..360 (ix) FEATURE: (A) NAME KEY: misc_feature (B) LOCATION: 1 (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1 1/2 heavy vhain variable region; amino acid 1 is Glu (E) but Gln (Q) may be substituted" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: GTC AAA CTG CAG CAG TCT QGG GCA GAG CTT GTG AAG CCA GGG GCC TCA 48 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser 1 5 GTC AAG TTG TCC TGC ACA GCT\TCT GGC TTC AAC ATT AAA GAC ACC TAT 96 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr 144 ATG CAC TGG GTG AAG CAG AGG CQT GAA CAG GGC CTG GAG TGG ATT GGA Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly 192 AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln 50 55 240 GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG Val Lys Ala Thr Ile Thr Ala Asp Thr\Ser Ser Asn Thr Ala Trp Leu 70 75 65 CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA 288 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 ,336 GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln 105 100 360 GGG ACC ACG GTC ACC GTC TCA Gly Thr Thr Val Thr Val Ser Ser 120 115 (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
20 25 30

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly

Arg lle Asp Pro Ala Ser Cly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
50 60

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
65 70 75 80

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser 115 120

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..318
 - (D) OTHER INFORMATION: /product = "HP1/2 light chain variable region"
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light chain variable region"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

48

96

10 15 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp 20 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA 144 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile \dagger AT TAT GCA \setminus TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC 192 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly 50 55 AGT\GGA TAT GGG\ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT 240 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala 65 70 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC 288 Glu Asp Leu Ala Val\Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr 85 ACG TTC GGA GGG GGG AQC AAG CTG GAG ATC 318 Thr Phe Gly Gly Gly That Lys Leu Glu Ile 100 (2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino \acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: prote\in (xi) SEQUENCE DESCRIPTION:\SEQ ID NO:4: Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly 10 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp 20 Val Ala Trp Tyr Gln Gln Lys Pro Gly Glh Ser Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala 65 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile 100 105

SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: Lobb, Roy R.
- (ii) TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 60 State Street, Suite 510
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/373,857
 - (B) FILING DATE: 18 JAN 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/284,603
 - (B) FILING DATE: 11-AUG-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/835,139
 - (B) FILING DATE: 12 FEB 1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US93/00924
 - (B) FILING DATE: 2-FEB-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Louis Myers (PLM)
 - (B) REGISTRATION NUMBER: 35,965
 - (C) REFERENCE/DOCKET NUMBER: BGP-031USCP
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS(B) LOCATION: 1..360
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| • | | | | | | | | | | | | | | | | | |
|------------|------------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|---|-----|
| | AAA Lys | | | | | | | | | | | | | | | | 48 |
| | AAG Lys | | | | | | | | | | | | | | | | 96 |
| ATG Met | CAC His | TGG Trp 35 | GTG Val | AAG Lys | CAG Gln | AGG Arg | CCT Pro 40 | GAA Glu | CAG Gln | GGC Gly | CTG Leu | GAG Glu 45 | TGG Trp | ATT Ile | GGA Gly | Ξ | 144 |
| | ATT Ile 50 | | | | | | | | | | | | | | | : | 192 |
| | AAG Lys | | | | | | | | | | | | | | | : | 240 |
| | CTC Leu | | | | | | | | | | | | | | | : | 288 |
| | GGA Gly | | | | | | | | | | | | | | CAA Gln | ; | 336 |
| | ACC Thr | | | | | | | | | | | | | | | | 360 |

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser 1 5 10 15
- Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr . 20 25 30
- Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
 35 40 45
- Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
 50 55 60
- Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu 65 . 70 . 75 . 80
- Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95
- Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
 100 105 110
- Gly Thr Thr Val Thr Val Ser Ser 115 120
- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..318
 - (D) OTHER INFORMATION: /product= "HP1/2 light chain variable region"
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light chain variable region"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
|------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------|---------------------|-------------------------------|----------------------------------|--------------------------------|-------------------------|---------------------------|--------------------------------|---------------------------------------|---------------------------------------|-------------------------|--------------------------------|-------------------------|--------------------------------|-----|
| | | | ACC Thr 20 | | | | | | | | | | | | | 96 |
| | | | TAC Tyr | | | | | | | | | | | | | 144 |
| | | | TCC Ser | | | | | | | | | | | | | 192 |
| | | | GGG Gly | | | | | | | | | | | | | 240 |
| | | | GCA Ala | | | | | | | | | | | | Tyr | 288 |
| | | | GGG Gly 100 | | | | | | | | | | | | | 318 |
| (2) | INFO | ORMA: | rion | FOR | SEQ | ID 1 | 10:4 | : | | | | | | | | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 106 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear | | | | | | | | | | | | | | | |
| | | | • | | | | | | | | | | | | | |
| | (: | Li) r | MOLE | CULE | TYPI | E: p | rote | in | | | | | | | | |
| | | | MOLE SEQUI | | | _ | | | Q ID | NO:4 | 1: | • | | | | |
| 1 | (z Ile | ki) s Val | SEQUI Met | ENCE Thr 5 | DES(| CRIP: | rion Pro | : SE(| Phe 10 | Leu | Leu | | | 15 | | |
| 1 | (z Ile | ki) S Val | SEQUI | ENCE Thr 5 | DES(| CRIP: | rion Pro | : SE(| Phe 10 | Leu | Leu | | | 15 | | |
| 1 Asp | (z Ile Arg | val Val | SEQUI Met Thr | Thr 5 | DESO | Thr Cys | Pro Pro Lys | : SE(Lys Ala 25 | Phe 10 Ser | Leu Gln | Leu Ser | Val | Thr 30 | 15 Asn | Asp | |
| 1 Asp Val | Ile Arg | val Val Trp 35 | Met Thr | Thr 5 Ile | Gln Thr | Thr Cys | Pro Lys Pro 40 | Lys Ala 25 Gly | Phe 10 Ser Gln | Leu Gln Ser | Leu Ser Pro | Val Lys 45 | Thr 30 Leu | 15 Asn Leu | Asp | |
| 1 Asp Val Tyr | Ile Arg Ala Tyr 50 | Val Val Trp 35 | Met Thr 20 | Thr 5 Ile Gln Asn | DESC Gln Thr Gln Arg | Thr Cys Lys Tyr 55 | Pro Lys Pro 40 | Lys Ala 25 Gly | Phe 10 Ser Gln Val | Leu Gln Ser Pro | Leu Ser Pro Asp | Val Lys 45 Arg | Thr 30 Leu | 15 Asn Leu Thr | Asp Ile Gly | |
| Asp Val Tyr Ser 65 | Ile Arg Ala Tyr 50 | Val Val Trp 35 Ala | Met Thr 20 Tyr | Thr 5 Ile Gln Asn | DESC Gln Thr Gln Arg | Thr Cys Lys Tyr 55 | Pro Lys Pro 40 Thr | Lys Ala 25 Gly Gly Phe | Phe 10 Ser Gln Val | Leu Gln Ser Pro Ile 75 | Leu Ser Pro Asp 60 Ser | Val Lys 45 Arg | Thr 30 Leu Phe Val | 15 Asn Leu Thr | Asp Ile Gly Ala 80 | |

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lobb, Roy R.
- (ii) TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease
- (iii) NUMBER OF SEQUENCES: 4
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 - (B) STREET: 60 State Street, Suite 510
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
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 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
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 - (B) FILING DATE: 18 JAN 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/284,603
 - (B) FILING DATE: 11-AUG-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/835,139
 - (B) FILING DATE: 12 FEB 1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US93/00924
 - (B) FILING DATE: 2-FEB-1993
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 - (A) NAME: Louis Myers (PLM)
 - (B) REGISTRATION NUMBER: 35,965
 - (C) REFERENCE/DOCKET NUMBER: BGP-031USCP
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..360 (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 1 (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy vhain variable region; amino acid 1 is Glu (E) but Gln (Q) may be substituted" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA 48 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser 5 GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT 96 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr 25 ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA 144 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly 192 AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG 240 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu 75 70 CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA 288 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala

336

360

110

Gly Thr Thr Val Thr Val Ser Ser 115

GGG ACC ACG GTC ACC GTC TCA

100

1

65

(2) INFORMATION FOR SEQ ID NO:2:

85

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids

GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln

105

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser

 1 10 15
- Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
 20 25 30
- Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly 35 40 45
- Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln 50 55 60
- Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu 65 70 75 80
- Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95
- Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
 100 105 110
- Gly Thr Thr Val Thr Val Ser Ser 115 120
- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..318
 - (D) OTHER INFORMATION: /product= "HP1/2 light chain variable region"
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light chain variable region"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
|-----------|---------------|------------------|------------|------------|------------------------|----------------|------------|-------------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----|
| | | GTT Val | | | | | | | | | | | | | | 96 |
| | | TGG Trp 35 | | | | | | | | | | | | | | 144 |
| | | GCA Ala | | | | | | | | | | | | | | 192 |
| | | TAT Tyr | | | | | | | | | | | | | | 240 |
| | | CTG Leu | | | | | | | | | | | | | | 288 |
| | | GGA Gly | | | | | | | | | | | | | | 318 |
| (2) | INFO | RMAT | rion | FOR | SEQ | ID 1 | NO:4: | : | | | | | | | | |
| | | (i) S | (A) | LEN TYI | CHAP IGTH: PE: & | : 106 amino | ami aci | ino a id | | 3 | | | | | | |
| | (ii) MOLECULE | | | | | _ | | | | | _ | | | | | |
| g., | | (i) S | _ | | | | | | - | | | 3707 | Cor | 77. | Cl. | |
| ser 1 | TTE | Val | | Thr 5 | | | Pro | | | | ьeu | Val | ser | 15 | GIY | |
| Asp | Arg | Val | Thr 20 | Ile | Thr | Cys | Lys | Ala 25 | Ser | Gln | Ser | Val | Thr 30 | Asn | Asp | |
| Val | Ala | Trp 35 | Tyr | Gln | Gln | Lys | Pro 40 | Gly | Gln | Ser | Pro | Lys 45 | Leu | Leu | Ile | |
| Tyr | Tyr 50 | Ala | Ser | Asn | Arg | Tyr 55 | Thr | Gly | Val | Pro | Asp 60 | Arg | Phe | Thr | Gly | |
| Ser 65 | Gly | Tyr | Gly | Thr | Asp 70 | Phe | Thr | Phe | Thr | Ile .75 | Ser | Thr | Val | Gln | Ala 80 | |
| Glu | Asp | Leu | Ala | Val 85 | Tyr | Phe | Cys | Gln | Gln 90 | Asp | Tyr | Ser | Ser | Pro 95 | Tyr | |
| Thr | Phe | Gly | Gly 100 | Gly | Thr | Lys | Leu | Glu 105 | Ile | | | | | | | |